



SEQUENCE LISTING

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Pedersen, Sven
Svendsen, Allan

<120> Fungamyl-like Alpha-Amylase Variants

<130> 5835.200-US

<140> US 09/710,339

<141> 2000-11-09

<150> US 60/165,786

<151> 1999-11-16

<160> 5

<170> PatentIn version 3.0

<210> 1

<211> 1734

<212> DNA

<213> Aspergillus Oryzae

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<221> CDS

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Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala Pro
5 10 15

gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc 152
Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe
20 25 30

ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg act 200
Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr
35 40 45

tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc 248
Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile
50 55 60 65

atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg	296
Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp	
70 75 80	
atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat	344
Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp	
85 90 95	
gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac	392
Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn	
100 105 110	
tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat gag	440
Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu	
115 120 125	
agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat	488
Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr	
130 135 140 145	
gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt	536
Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser	
150 155 160	
tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat	584
Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp	
165 170 175	
cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg	632
Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu	
180 185 190	
cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac	680
Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp	
195 200 205	
tgg gtg gga tca ttg gta tgc aac tac tcc att gac ggc ctc cgt atc	728
Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile	
210 215 220 225	
gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa	776
Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys	
230 235 240	
gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc	824
Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala	
245 250 255	
tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc	872
Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro	
260 265 270	

B'
cont.

att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg 920
 Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met
 275 280 285

gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac 968
 Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp
 290 295 300 305

tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc 1016
 Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe
 310 315 320

gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc 1064
 Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe
 325 330 335

atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag 1112
 Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln
 340 345 350

cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc 1160
 His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu
 355 360 365

tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg 1208
 Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala
 370 375 380 385

aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg acc 1256
 Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr
 390 395 400

tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc 1304
 Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg
 405 410 415

aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt 1352
 Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly
 420 425 430

gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca 1400
 Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr
 435 440 445

gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt 1448
 Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val
 450 455 460 465

ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg 1496
 Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg
 470 475 480

B¹
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gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt agc 1544
 Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser
 485 490 495

tcg tgaaggggtgg agagtatatg atggtactgc tattcaatct ggcattggac 1597
 Ser

agtgagtttg agtttgatgt acagttggag tcgttactgc tgatcatcccc ttatactctt 1657

cgattgtttt tcgaacccta atgccaagca cgctagtcta ttataggaaa aaaaaaaaaa 1717

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 <212> PRT
 <213> Aspergillus Oryzae

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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
 35 40 45

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
 50 55 60

Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
 65 70 75 80

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
 85 90 95

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
 100 105 110

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
 115 120 125

6'
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Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
130 135 140

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145 150 155 160

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
165 170 175

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
180 185 190

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
195 200 205

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
210 215 220

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225 230 235 240

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
245 250 255

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
260 265 270

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
275 280 285

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
290 295 300

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305 310 315 320

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
325 330 335

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
340 345 350

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
355 360 365

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
370 375 380

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385 390 395 400

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
405 410 415

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
420 425 430

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
435 440 445

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
450 455 460

Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465 470 475 480

Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
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Ser Ser

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 Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
 35 40 45
 Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
 50 55 60
 Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
 65 70 75 80
 Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
 85 90 95
 Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
 100 105 110
 Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
 115 120 125
 Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
 130 135 140
 Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
 145 150 155 160
 Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
 165 170 175
 Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
 180 185 190
 Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
 195 200 205
 Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
 210 215 220
 Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
 225 230 235 240
 Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
 245 250 255
 Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
 260 265 270

B'
 cont.

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
275 280 285

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
290 295 300

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305 310 315 320

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
325 330 335

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
340 345 350

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
355 360 365

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
370 375 380

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
385 390 395 400

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
405 410 415

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
420 425 430

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
435 440 445

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
450 455 460

Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
465 470 475 480

Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
485 490 495

Ser Ser

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27

B'
corel.